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RESEARCH ARTICLE

GENETIC ESTIMATES THROUGH NARROW SENSE HERITABILITY FOR SEVEN QUANTITATIVE TRAITS OF THE SILKWORM *BOMBYX MORI* L.

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Abstract

An investigation was undertaken to study the narrow sense heritability (h^2) of eighteen genotypes of the silkworm *Bombyx mori viz.*, six each of bivoltines- C_{108}, Kalimpong-A (KA), NB_4D_2, CSR_2, P_{31}, NB_{18}, multivoltines- Pure Mysore (PM), Nistari, *C.nichi*, MU_1, *npnd*, Hosa Mysore (HM) and mutants- zebra, ursa, knobbed, pere, lemon and *pre* drawn from the Germplasm Bank of Department. The scientific method of rearing was followed by analyzing seven quantitative traits *viz.*, larval weight, cocoon weight, cocoon shell weight, cocoon shell ratio, filament length, denier and renditta during three seasons (pre-monsoon, monsoon and post monsoon). The phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV) and h^2 were estimated for the seven of the above said quantitative traits in the eighteen races/breeds and mutants and relevant statistical procedures were utilized to compute the data generated.

The data pertaining to the mean values has revealed differential rearing performances of the eighteen races/breeds possibly because of their voltinistic differences. Based on the h^2 among six each of bivoltines, multivoltines and mutants, it is evident that the four traits namely larval weight, cocoon weight, denier and renditta recorded moderate h^2 values. On the other hand, the traits like filament length, shell weight and shell percentage revealed low heritability values during three seasons of the year. The moderate heritability values recorded by all the races/breeds showed that these characters can be further improved through phenotypic selection in the breeding programme indicating the contributions of additive action of genes and interestingly some of the mutant stocks can be utilized to enhance the selection for the breeding programmes are also herein discussed.

INTRODUCTION

The silkworm *Bombyx mori* a holometabolous lepidopteron insect is known for production of fabulous silk/fiber. The silkworm *Bombyx mori*, in the course of its development and the process of continuous rearing has undergone evolution through mutation, natural and artificial selection and today there are large number of races and strains found in different parts of the world. Besides, the silkworm breeders also have evolved a number of breeds by the process of hybridization with specific objectives of improvement of desired traits like, resistance to poor environment, increase in the length of silk filament, finer denier, improvement in the quality cocoon for higher shell ratio of raw silk and obtaining higher degree of evenness and neatness[1, 2]. Moreover, such a study has gained the

momentum through application of heritability studies to understand the genetic pattern of inheritance of selected races. Nevertheless, 'heritability' was originally defined by Lush,[3] as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects and this is now termed "heritability in the narrow sense" and is designated as "h^2"[4]. Thus, it is opined that heritability estimates act as an important yardstick in selection techniques for the improvement of qualitative and quantitative traits of the plants and animals[5]. Apart, the conventional method of determining the optimal selection environment is to estimate the efficacy of selection at one site for planting at another site, using method of indirect selection described by Falconer,[5]. Furthermore, in order to estimate the efficiency of selection, heritabilities and genetic correlations need to be known. Moreover, few selection criteria are dependent on breeders to better the best and breeding strategies are successful only when pattern of inheritance of economic traits are clearly understood with the background knowledge of gene-environmental interactions. One of the quickest means to get an insight into the depth of gene-environmental interaction is h^2. Heritability is useful to study the genetic change of a population undergoing selection and to choose among alternative breeding[6,7]. The offspring-parent regression is a widely used as estimator of h^2 that is simple to compute and is unbiased even when selection of parents occurs and the heritability is the only method that has been proved to be unbiased in the presence of selection[8].

Based on the existing studies both in plants and animals, it is clear that low heritability for a particular trait is mainly influenced by the environment and higher heritability for some characters may be due to relatively low environmental influence for the traits[9]. In silkworm *Bombyx mori*, heritability estimates are elaborately applied for selecting the best individuals to step up further selection[10,15]. Further, the Jolly *et al.*[16] and Siddiqui *et al.*[17] reported genotypic and phenotypic variability for some quantitative traits in non mulberry Tasar silkworms. However, heritability studies are very important to understand the nature of inheritance of qualitative and quantitative traits and to predict the genetic variation due to complete domestication and continuous selection during different seasons for mulberry silkworm to extrapolate results in breeding programme. Keeping the above aspects in view, the present investigation was undertaken to understand the genetic variability for seven quantitative traits through h^2 during three seasons of the year by utilizing the different races, breeds and mutants of the silkworm *Bombyx mori*.

MATERIALS AND METHODS

Narrow sense heritability was computed for seven quantitative traits *namely*., larval weight, cocoon weight, shell weight, shell percentage, filament length, denier and renditta utilizing ten pure races, which include five bivoltines (C_{108}, Kalimpong-A (KA), NB_4D_2, P_{31} & NB_{18}) and five multivoltines (Pure Mysore, Nistari, C.nichi, *npnd* & Hosa Mysore) two evolved breeds each one belonging to multivoltine (MU_1) and bivoltine (CSR_2) and six mutants *viz.*, zebra, ursa, knobbed, *pere* (pink eyed red eggs*)* lemon and *pre* (Precocity). The description of the morphological features is presented in Table-1.

The parental seed cocoons of the above said eighteen races/breeds and mutants were collected from the Germplasm Bank of Department of Studies in Sericulture, University of Mysore and layings were prepared and reared by adopting the methods described by Tazima and Krishnaswami,[18,19] respectively. For heritability studies, three replications each of twenty five male and twenty five female larvae were maintained and the fifth instar larvae from all the replicates were selected a day before spinning and their larval weight was recorded after labeling them. Simultaneously, each labeled larvae were individually left on the mountages (in a manual made paper box with proper aeration for spinning the good cocoons). The cocoons harvested were assessed for seven quantitative traits by following the standard method described by Mather and Jinks,[20] with mean, Phenotypic co-efficient variability (PCV), Genotypic co-efficient variability (GCV) and Narrow sense heritability (h^2) percentage was calculated through the Genstat 9th version (2008) statistical package utilizing the formula as detailed below:

$$H^2 \text{ (or } h^2N) = \frac{V_A}{V_P} = \frac{V_A}{V_G + V_E}$$

Where,

H^2 = Narrow sense heritability

V_A = Additive variance
V_P = Phenotypic variance
V_G = Genetic variance
V_E = Environmental variance.

Table 1: Description of four qualitative traits in six each of bivoltine, multivoltine races/breeds and mutants of the silkworm *Bombyx mori.*

Characters / Races/breeds	Voltinism	Origin	Larval pattern	Cocoon colour	Cocoon shape
C_{108}	Bivoltines	China	Plain	White	Oval
KA		India	Plain	White	Oval
NB_4D_2		India	Plain	White	Dumb-bell
CSR_2		India	Plain	White	Oval
P_{31} Bione		European	Marked	White	Dumb-bell
NB_{18}		India	Plain	White	Dumb-bell
PM	Multivoltines	India	Plain	Light green	Spindle
Nistari		India	Marked	Golden yellow	Spindle
C.nichi		Japan	Plain	White	Dumb-bell
MU_1		India	Plain	Green	Oval
Npnd		Japan	Marked	White	Oval
HM		India	Plain	Dark green	Oval
Zebra	Bivoltine mutants	Japan	Marked	White	Dumb-bell
Ursa		Japan	Marked	White	Dumb-bell
Knobbed		Japan	Plain	White	Dumb-bell
Pere		Japan	Marked♀♀ Plainðð	White	Dumb-bell
Lemon		Japan	Plain	White	Dumb-bell
Pre	Multivoltine mutant	Japan	Marked	White	Oval

RESULTS

The data pertaining to statistically analyzed results of the PCV, GCV and h^2 for the seven quantitative traits during pre-monsoon, monsoon and post-monsoon seasons among six each of bivoltine, multivoltine and mutant are presented in Figs. 1-9. Apart, the average of three season's results among six bivoltine races/breed of the silkworm *Bombyx mori* are presented in Table -2 and depicted in Figure-10. From the observation for the trait larval weight it is clearly indicative that, a highest PCV (1.05) and GCV (0.39) were noticed in CSR_2 and NB_4D_2 breeds respectively, on the other hand, a lowest PCV (0.85) and GCV (0.36) were recorded in NB_4D_2 race alone. The data of h^2 estimate showed that, an highest h^2 percentage of 46.24 value was observed in NB_4D_2 race, where as a lowest of 36.34 was recorded in CSR_2 breed. The trait cocoon weight, an highest PCV value of 1.03 was evident in NB_{18} race, where as a least of 0.91 was observed in CSR_2 breed and GCV higher value (0.44) was recorded in NB_{18}, where as lowest of 0.34 was evident in KA race. The h^2 values showed that, an highest of 43.24 was shown by NB_{18} race, where as a lowest h^2 of 36.04 was evident in KA race and remaining four races have revealed the value in

between the above two races. The data in regard to the trait shell weight during same season, an highest PCV value of 1.03 was evident in NB_4D_2 and lowest of 0.88 was noticed in CSR_2 breed and GCV value of 0.45 was alone exhibited by C_{108} and NB_{18} races. The h^2 recorded an highest of 47.97 which is evident in C_{108} race followed by CSR_2 with 47.46, NB_{18} with 45.36, KA with 41.52, P_{31} with 39.46 and NB_4D_2 with 37.32. For the traits shell ratio and filament length it is clear from the data that, an highest PCV values of 1.05 and 1.01 were observed in NB_4D_2 and NB_{18} races respectively, where as GCV values of 0.44 0.45 were noticed in CSR_2 and NB_{18} respectively. The h^2 values revealed a lowest percentage of 38.07 and 28.27 exhibited by P_{31} races alone and highest h^2 values of 47.39 and 46.38 were noticed in CSR_2 breed alone. The data with regard to the traits denier and renditta, the higher PCV (0.99 and 1.05) and GCV (0.45 and 0.46) were noticed in NB_{18}, NB_4D_2 and CSR_2 races/breed respectively. The h^2 values of 48.80 (KA) and 47.79 (CSR_2) which are highest and h^2 values of 33.04 (P_{31}) and 37.48 (C_{108}) which are lowest and remaining races have exhibited moderate h^2 values.

Further, the data pertaining to PCV, GCV and narrow sense heritability presented in percentages during three seasons among six multivoltine races/breed of the silkworm *Bombyx mori* (Table-3 & Figure-11). From the data it is clear that for the trait larval weight, an highest PCV (0.99) and GCV (0.47) were exhibited by MU_1 breed alone. The data relevant to h^2 estimates showed that, an highest h^2 percentage of 47.98 was recorded by Hosa Mysore, where as a lowest h^2 percentage of 34.21 was observed in the Pure Mysore. For the trait cocoon weight during same seasons, an higher PCV and GCV values of 1.07 and 0.36 were revealed by *npnd* and MU_1 race/breed respectively. Similarly, an highest percentage of 39.25 value was noticed by Pure Mysore race followed by 38.99 in MU_1, 37.67 in Hosa Mysore, 33.07 in *npnd*, 32.36 in Nistari and 30.42 in C.nichi race. It is very interesting to note that for the traits shell weight and shell ratio, maximum PCV and GCV values of 0.97, 00.93 and 0.34, 0.33 were recorded in MU_1 and Pure Mysore races/breed respectively. Further same two traits h^2 values highest of 38.02 and 39.52 were exhibited by Hosa Mysore race alone, where as a lowest values of 28.58 and 24.15 were evident by *npnd* race alone. For the trait filament length it is indicative that, higher PCV (1.00) and GCV (0.33) were recorded in C.nichi and Hosa Mysore races respectively. For h^2 values, a highest percentage of 36.54 value was recorded in Hosa Mysore followed by MU_1 (34.65), Pure Mysore (34.68), Nistari (28.85), C.nichi (26.46) and *npnd* (23.93) races. The data with respect to the traits denier and renditta, an higher PCV (1.00, 1.02 in *npnd*, Nistari) and GCV (0.44, 0.39 in MU_1 breed alone) was recorded among six multivoltines. The data of h^2 showed that, an highest values of 43.97 and 44.43 were exhibited by MU_1 breed alone for two traits of denier and renditta, where as a lowest of 31.15 and 36.73 was noticed in *npnd* and Nistari races respectively.

However, the data pertaining to average PCV, GCV and narrow sense heritability in the six mutant stocks during three seasons is presented in the Table-4 & Figure-12. The data for the traits larval weight and cocoon weight, it is clearly indicative that, lowest PCV values of 0.92 and 0.90 were exhibited by ursa mutant, where as a highest PCV values of 0.99 and 1.01 were noticed in zebra mutant. The GCV values for the same traits revealed higher of 0.44 and 0.46 in zebra mutant, where as a lower GCV values of 0.27 and 0.29 were observed by lemon mutant alone. The h^2 values for the same traits revealed lowest of 28.29 and 32.38 were recorded by lemon mutant, where as an highest of 46.21 and 47.46 in knobbed mutant. For the trait shell weight, highest PCV and GCV values of 0.99 and 0.45 were exhibited by knobbed mutant and a lowest h^2 value of 35.74 was evident in *pre* mutant, where as an highest of 45.28 was revealed by knobbed mutant. It is evident from the table for the trait shell ratio, higher PCV (0.96) and GCV (0.45) were recorded in *pere* and knobbed mutants respectively, where as lower values of 0.86 and 0.31 were noticed in *pre* and ursa mutants respectively. The h^2 values recorded a lowest of 34.55 in pere mutant, where as an highest value of 46.46.47 was noticed in knobbed mutant. For the trait filament length, a maximum PCV and GCV values of 0.97 and 0.42 were found in knobbed mutant alone, where as minimum values of 0.91 and 0.33 were shown in *pre* and lemon mutants respectively. The data of h^2 estimates showed that, an highest value of 44.09 was recorded by knobbed followed by pere with 40.01, ursa with 38.49, *pre* with 38.34, zebra with 36.57 and lemon with 34.75. The data in regard to the two traits denier and renditta revealed that, the higher percentage of PCV values of 1.05 and 1.04 were exhibited by lemon and zebra mutants respectively and GCV values of 0.44 alone was recorded in knobbed mutant alone. The h^2 values shown that, highest values of 45.57 and 47.08 were exhibited by knobbed mutant alone, where as lowest h^2 values of 31.50 and 30.75 were evident in lemon and *pre* mutants respectively.

DISCUSSION

Generally hybridization followed by rigid selection is considered as an important procedure in enhancing the selection gain for the selected traits both in animal and plant breeding programmes. It is considered opinion of livestock breeders that systematic selection alone and application of popular biometrical procedures will result in the

superior progenies. Lush[3] opined that selection of beneficial traits will enhance the selection gain in any population. It is proposed that the biometrical genetics knowledge in any conventional breeding programmes will result in the superior progenies[21]. Further, Kempthorne[22] and Falconer[5] successfully developed several biometrical methods in the livestock breeding programs and richly contributed for the linear growth of livestock production. Keeping this in view the Bell *et al.*[23] opined that improved techniques of animal breeding will minimize the accumulation of deleterious genes. Moreover, the pioneering work of Falconer[5], in lab mice clearly demonstrated that heritability estimation is of utmost importance to understand gene environmental interaction in any populations. But it is interesting to understand how best environmental condition expresses the heritability traits among unknown genotypes.

The observed data in the present experiment with respect to the two traits namely denier and renditta, wherein an highest PCV values (1.00, 1.02 in *npnd*, Nistari) and GCV (0.44, 0.39 in MU_1 breed alone) were recorded among six multivoltines. The data of h^2 showed that, an highest values of 43.97 and 44.43 were exhibited by MU_1 breed alone for two traits of denier and renditta, where as a lowest of 31.15 and 36.73 were noticed in *npnd* and Nistari races respectively. Such a variable result being considered as influence of various factors, further above observation reflects that the phenotypic manifestation of any genetically controlled traits is a product of interaction between the genotype and the ambient environment. It is important to note that even in the pre-monsoon season, some of the races/breeds exhibited higher range of narrow sense heritability values suggesting that the role of environmental factors are less than the genotype. The above studies corroborate with the findings of Narasimhanna[24] in bivoltine races, in temperate bivoltine races[13] and in the evolved bivoltine lines[25-28].

Perusal of literatures in silkworm shows that the heritability estimation for various quantitative traits revealed different degree of heritability values based on the aboriginal features of different races of the silkworm, *Bombyx mori* and the results are very well documented. The investigators like Tsuchiya and Kurashima[29] have reported heritability values for cocoon shell weight, cocoon filament weight; cocoon filament size and cocoon filament length to be 68, 51, 54 and 71% respectively in Japanese and Chinese hybrids. From their reports it is evident that the heritability of the characters was higher in the female than in the males in the hybrid population. Further, it is demonstrated that, the expression of productivity depends on the magnitude of genetic variability and the extent to which the associated traits are heritable in silkworm[30]. As pointed out various researchers that, the characters within moderate heritability ranging from 31-70 percentage are more flexible and the contributions of the additive genetic variance is about twice as much as the non additive genetic variations, which means poor non additive genetic variation for the expression of the above characters[13,24,25,26, 27,31]. However, based on the variable expression of moderate heritability values in the eighteen selected races/breeds and mutants, considering the genetic and environmental interactions involved in the expression of these characters, it is opined that because of the genetic homogeneity for the dominant genes with least over-dominance effect the possibility of recording moderate heritability estimates which are observed in the present findings cannot be ruled out. Moreover, the Gamo and Hirabayashi[32], reported that the feeding seasons had a considerable influence on the phenotypic expression and value for co-efficient of heritability varies greatly for cocoon weight, weight of the silk, shell thickness of the raw cocoons. It is reported that, the phenotypic and genotypic variance and co-efficient of variance, variance in the broad sense and genetic gain for nineteen quantitative traits in a study of four bivoltine strains of *Bombyx mori* and their single and double cross hybrids[14],.

Further, Giridhar *et al.*[33] demonstrated that the cocoon weight, shell weight, filament length and denier can be considered as the criteria for selection for the improvement of cocoon yield. Thus, based on the results from the findings presented in the above said tables, it is obvious that the magnitude of heritability depends on the complexity of traits and the range of heritability values is an index of additive genetic variation, non-additive genetic variation and over-dominance effects. The overall picture that emerges out of the findings of heritability clearly indicates that bivoltines with superior economic traits revealed low percentage of heritability than mutant stocks. Thus it is opined by the present investigators that some of the mutant stocks can be utilized in the breeding programme in order to enhance the selection. Moreover, the moderate h^2 observed in the races/breeds showed that these characters can be further improved through phenotypic selection in the breeding programme indicating the contributions of additive action of genes. In addition, the present experimental data will serve an important yardstick to understand the genotypic and environmental interaction and helpful in silkworm genetics, hybridization and breeding programmes.

Table-2 Narrow sense heritability for seven quantitative traits (Average of three seasons) in the six bivoltine races/breed of the silkworm *Bombyx mori*

Races / Traits	C_{108}				Kalimpong-A				NB_4D_2			
	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)
Larval Weight (g)	38.58±0.056	0.94	0.38	40.82	38.48±0.53	0.95	0.37	40.27	37.15±0.62	0.85	0.39	46.24
Cocoon Weight (g)	1.98±0.050	1.02	0.39	37.61	1.5±0.48	0.96	0.34	36.04	1.79±0.57	0.95	0.40	42.74
Shell Weight (g)	0.360±0.021	0.94	0.45	47.97	0.28±0.052	0.96	0.39	41.52	0.326±0.056	1.03	0.38	37.32
Shell ratio (%)	18.15±0.020	0.93	0.39	44.12	18.51±0.046	0.92	0.39	42.39	18.04±0.043	1.05	0.39	38.27
Filament length (m)	912.66±1.64	0.82	0.34	42.50	908±0.66	0.98	0.39	40.71	3601±0.33	0.98	0.43	43.75
Denier	2.33±0.006	0.92	0.39	41.87	2.24±0.025	0.92	0.45	48.8	2.31±0.035	0.97	0.35	37.04
Renditta	7.67±0.026	1.03	0.39	37.48	6.44±0.035	1.01	0.46	46.20	8.38±0.042	1.05	0.45	43.26
Races/breed / Traits	**CSR_2**				**P_{31}**				**NB_{18}**			
	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)
Larval Weight (g)	41.54±0.045	1.05	0.38	36.34	38.34±0.53	0.87	0.36	43.02	40.78±0.45	0.93	0.37	39.64
Cocoon Weight (g)	2.11±0.040	0.91	0.40	43.03	1.56±0.36	0.97	0.35	36.61	1.780±0.031	1.03	0.44	43.24
Shell Weight (g)	0.40±0.031	0.88	0.42	47.46	0.28±0.043	0.93	0.36	39.46	0.31±0.034	1	0.45	45.36
Shell ratio (%)	19.82±0.025	0.93	0.44	47.39	18.04±0.035	0.94	0.36	38.07	17.74±0.026	0.98	0.44	45.41
Filament length (m)	1056±2.066	0.97	0.45	46.38	903.66±0.64	0.86	0.24	28.27	3671±0.65	1.01	0.44	43.99
Denier	2.31±0.024	0.93	0.45	46.08	2.27±0.025	0.93	0.32	33.04	2.31±0.026	0.99	0.44	44.32
Renditta	7.15±0.030	0.95	0.46	47.79	5.8±0.034	0.94	0.36	38.7	6.24±0.034	1	0.45	45.60

Index: SE= Standard error, **PCV=** Phynotypic co-efficient variability, **GCV=** Genotypic co-efficient variability, **h^2=** Narrow sense heritability, **%=** Percentage, **g** =Gram and **m** =mitre.

Table-3 Narrow sense heritability for seven quantitative traits (Average of three seasons) in the six multivoltine races/breed of the silkworm *Bombyx mori*

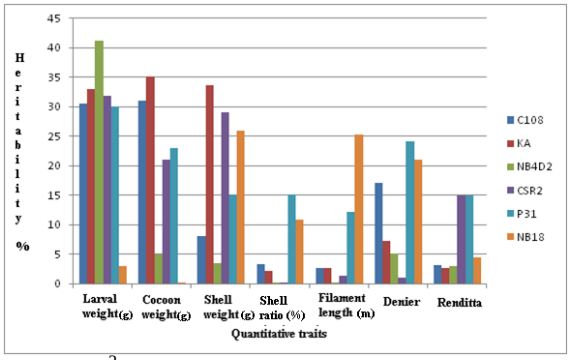
Races / Traits	Pure Mysore				Nistari				C.nichi			
	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)
Larval Weight (g)	20.60±0.052	0.96	0.33	34.21	21.88±0.53	0.96	0.36	38.05	17.39±0.56	0.95	0.33	35.58
Cocoon Weight (g)	1.02±0.033	0.9	0.35	39.25	0.93±0.35	0.98	0.30	32.36	0.9±0.46	0.92	0.28	30.42
Shell Weight (g)	0.13±0.033	0.97	0.33	35.02	0.12±0.042	0.97	0.32	32.98	0.10±0.066	0.94	0.32	36.2
Shell ratio (%)	13.42±0.032	0.93	0.33	36.28	13.18±0.034	0.84	0.25	30.08	11.17±0.033	0.87	0.23	26.46
Filament length (m)	355±1.064	0.89	0.31	34.68	348±0.33	0.99	0.28	28.85	489±0.67	1	0.26	26.22
Denier	1.92±0.017	0.92	0.29	31.74	1.99±0.026	0.88	0.36	40.30	1.99±0.033	0.95	0.34	35.34
Renditta	12.06±0.033	0.93	0.35	37.64	11.10±0.025	1.02	0.38	36.73	12.14±0.025	0.87	0.25	29.19
Races/breed / Traits	**MU_1**				***npnd***				**Hosa Mtsore**			
	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)
Larval Weight (g)	25.85±0.033	0.99	0.47	47.98	15.73±0.53	0.98	0.34	34.44	25.99±0.67	0.95	0.46	47.98
Cocoon Weight (g)	1.14±0.067	0.92	0.36	38.99	0.85±0.35	1.07	0.36	33.07	1.09±0.35	0.88	0.34	37.67
Shell Weight (g)	0.18±0.053	0.95	0.34	36.44	0.099±0.34	0.91	0.26	28.58	0.178±0.053	0.86	0.32	38.02
Shell ratio (%)	16.17±0.067	0.81	0.31	39.42	11.69±0.025	0.96	0.23	24.15	16.47±0.053	0.79	0.31	39.52
Filament length (m)	551.66±1.67	0.92	0.32	34.65	270±0..39	0.97	0.24	23.93	549±0.66	0.90	0.33	36.54
Denier	2.15±0.033	0.99	0.44	43.97	1.95±0.025	1.00	0.31	31.15	2.05±0.028	0.89	0.34	39.01
Renditta	11.44±0.025	0.913	0.39	44.43	13.62±0.024	0.94	0.35	38.43	11.99±0.034	0.92	0.37	39.75

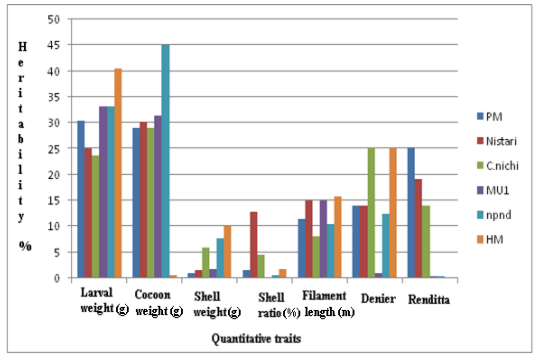
Index: SE= Standard error, **PCV=** Phynotypic co-efficient variability, **GCV=** Genotypic co-efficient variability, **h^2=** Narrow sense heritability, **%=** Percentage, **g** =Gram and **m** =mitre.

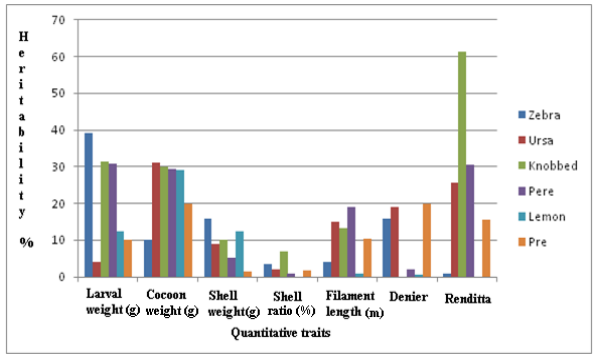
Table-4 Narrow sense heritability for seven quantitative traits (Average of three seasons) in the six mutant stocks of the silkworm *Bombyx mori*

Mutants / Traits	zebra				ursa				knobbed			
	Mean ± SE	PCV %	GCV %	h^2 %	Mean ± SE	PCV %	GCV %	h^2 %	Mean ± SE	PCV %	GCV %	h^2 %
Larval Weight (g)	37.75±0.056	0.99	0.42	42.35	37.25±0.62	0.92	0.43	48.33	28.72±0.33	0.98	0.44	46.21
Cocoon Weight (g)	1.72±0.066	1.01	0.38	37.75	1.72±0.033	0.9	0.38	41.89	1.52±0.33	0.97	0.46	47.46
Shell Weight (g)	0.273±0.053	0.98	0.38	37.68	0.24±0.067	0.8	0.37	41.28	0.25±0.67	0.99	0.45	45.28
Shell ratio (%)	15.65±0.033	0.95	0.32	37.37	14.24±0.065	0.87	0.31	36.38	16.53±0.039	0.96	0.45	46.47
Filament length (m)	346±2.033	0.95	0.35	36.57	347.33±1.033	0.94	0.36	38.49	351±0.67	0.97	0.42	44.09
Denier	2.35±0.026	0.83	0.43	45.59	2.25±0.033	0.98	0.34	34.49	1.91±1.028	1.00	0.44	45.57
Renditta	11.61±0.066	1.04	0.36	35.63	11.2±0.024	0.99	0.41	41.23	11.10±0.03	0.94	0.44	47.08
Mutants / Traits	**pere**				**lemon**				***pre***			
	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)	Mean ± SE	PCV (%)	GCV (%)	h^2 (%)
Larval Weight (g)	38.00±0.33	0.97	0.41	42.95	22.98±0.67	0.94	0.27	28.29	17.52±0.64	0.98	0.3	29.4
Cocoon Weight (g)	1.836±0.67	0.92	0.36	39.29	1.343±0.33	0.93	0.29	32.38	1.08±0.67	0.96	0.34	35.54
Shell Weight (g)	0.29±0.063	0.93	0.36	38.62	0.206±0.66	0.95	0.36	37.19	0.16±0.33	0.88	0.31	35.74
Shell ratio (%)	16.1±0.025	0.96	0.33	34.55	15.27±0.027	0.93	0.336	34.88	14.92±0.034	0.86	0.32	36.38
Filament length (m)	415±2.062	0.94	0.37	40.01	352.66±1.067	0.96	0.33	34.75	332±1.33	0.91	0.34	38.34
Denier	2.30±0.033	0.96	0.34	35.25	1.90±0.067	1.05	0.33	31.50	1.9±0.026	0.85	0.34	39.89
Renditta	10.94±0.025	0.98	0.37	37.55	11.15±0.025	1.01	0.36	35.51	11.32±0.28	0.95	0.28	30.75

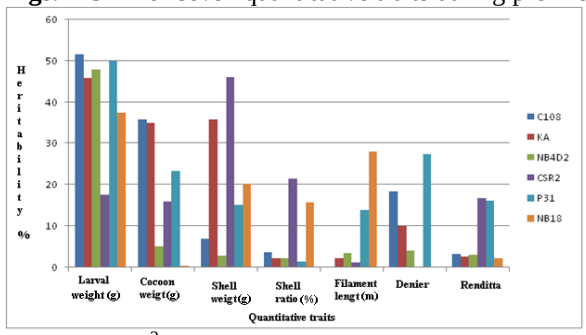
Index: SE= Standard error, **PCV=** Phynotypic co-efficient variability, **GCV=** Genotypic co-efficient variability, **h^2=** Narrow sense heritability, **%=** Percentage, **g =**Gram and **m =**mitre.

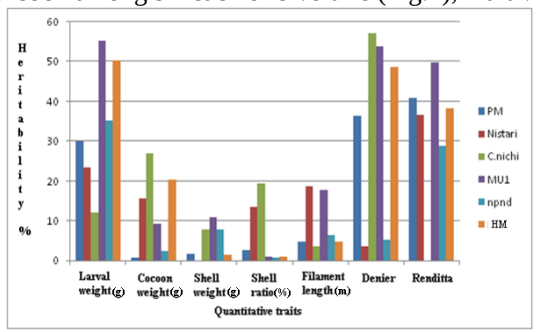


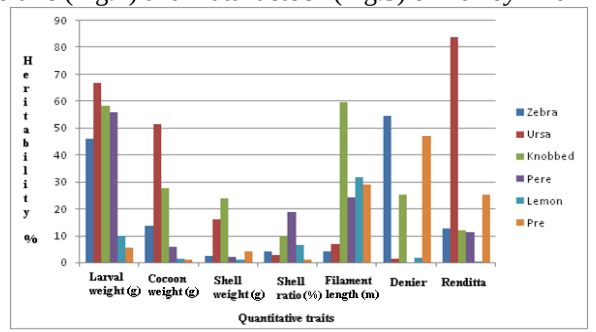




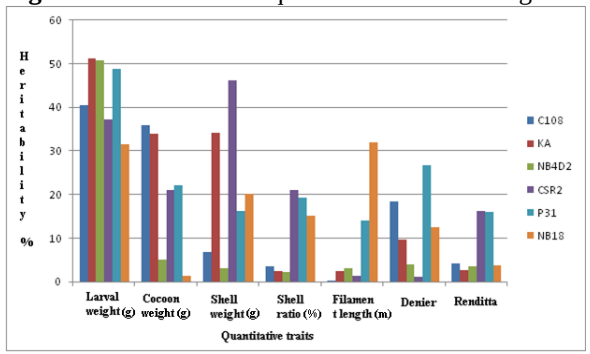
Figs.-1-3 h^2 for seven quantitative traits during pre-monsoon among six each of bivoltine (Fig.1), multivoltine (Fig.2) and mutant stock (Fig.3) of *Bombyx mori*

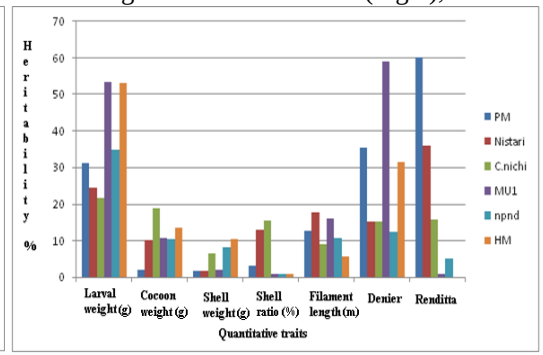


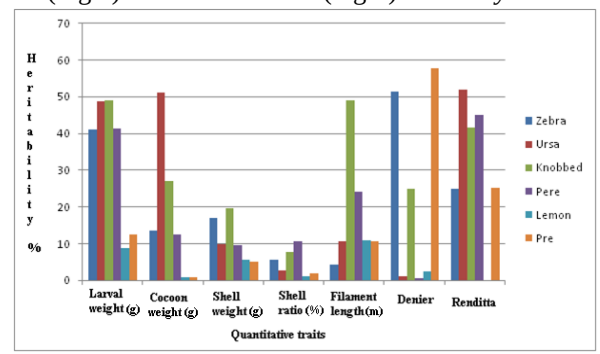




Figs.-4-6→ h^2 for seven quantitative traits during monsoon among six each of bivoltine (Fig.4), multivoltine (Fig.5) and mutant stock (Fig.6) of *Bombyx mori*







Figs.7-9→ h^2 for seven quantitative traits during post-monsoon among six each of bivoltine (Fig.7),multivoltine (Fig.8) and mutant stock (Fig.9) of *Bombyx mori*

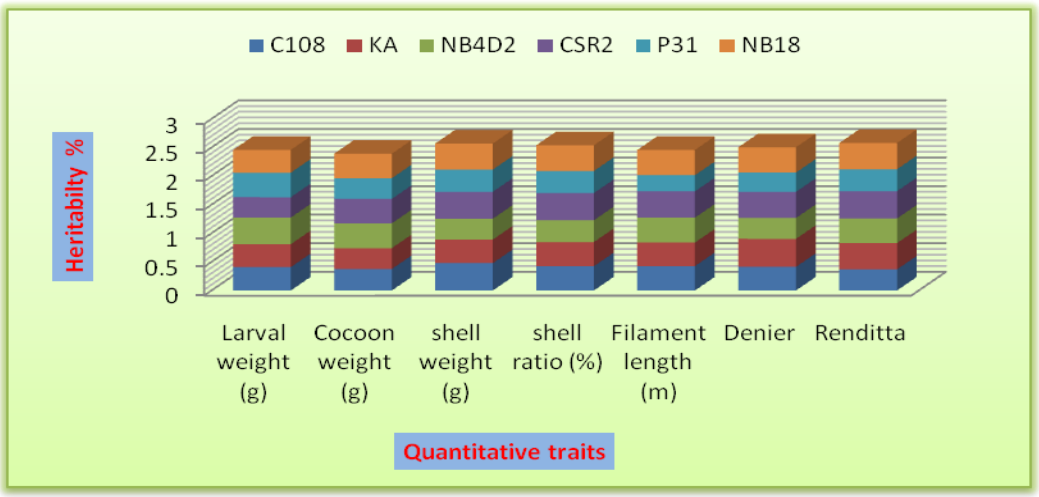


Fig.10: h^2 for seven quantitative traits (Average of three seasons) among six bivoltine races/breed of the *Bombyx mori*

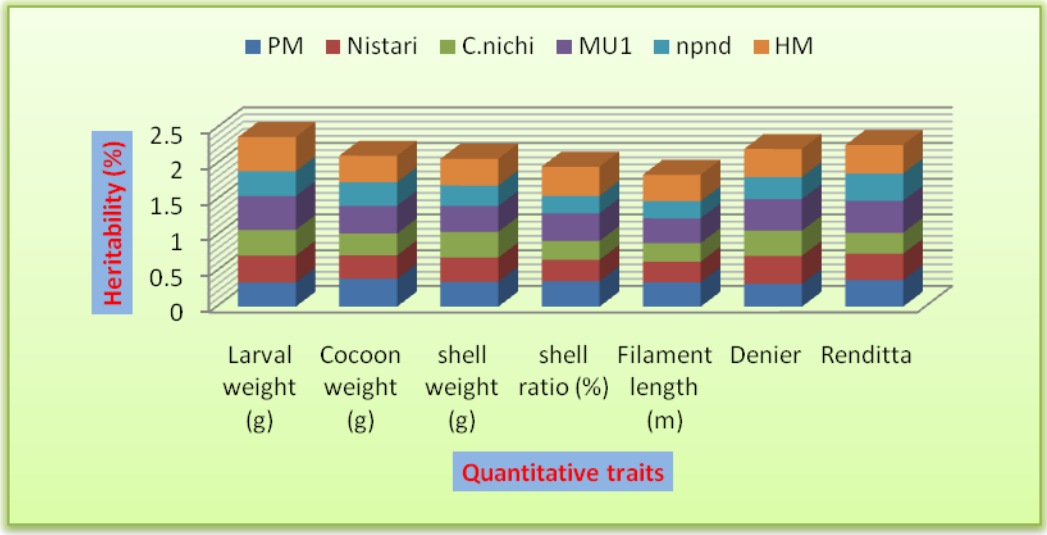


Figure-11: h^2 for seven quantitative traits (Average of three seasons) among six multivoltine races/breed of the *Bombyx mori*

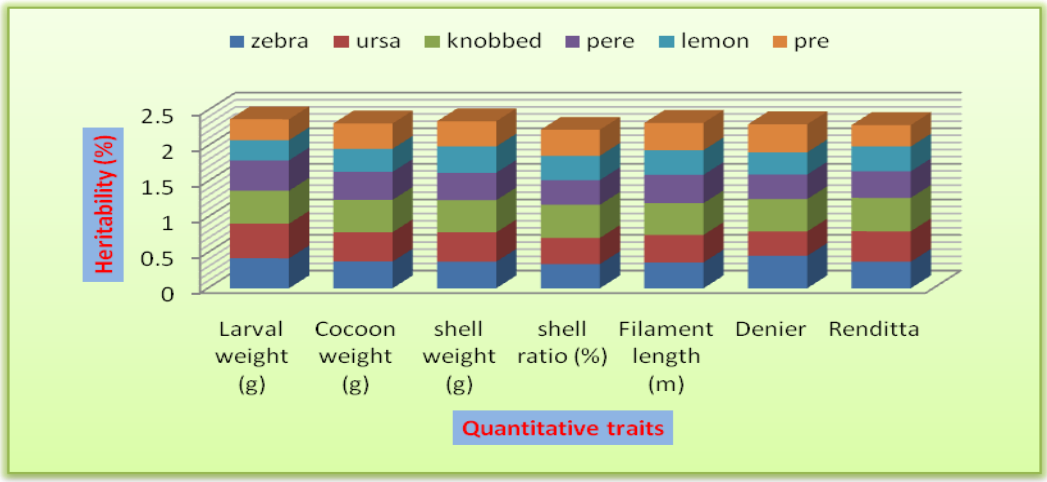


Fig.-12: h^2 for seven quantitative traits (Average of three seasons) among six mutant stocks of the *Bombyx mori*

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